In the specification at page 60, line 26, please add the following:

A2

-- As disclosed in US patent 5,445,934 arrays with nucleic acid molecules can comprise a substrate with a surface comprising 10^3 or more groups of oligonucleotides with different, known sequences covalently attached to the surface in discrete known regions, *e.g.*, 10^4 or 10^5 or 10^6 or more different groups of known sequences in discrete known regions. In preferred arrays 10^3 or more groups of oligonucleotides occupy a total area of less than 1 cm^2. In preferred embodiments the groups of oligonucleotides are at least 50% pure within the discrete known regions. --

REMARKS

Support for new claims 8-11, which are directed to a single invention, is found in the specification as originally-filed. In particular, see pages 59-61 for a general discussion of arrays and microarrays, including incorporated references, especially US Patent 5,445,934, columns 31 and 32; pages 12-15 for methods adaptable for arrays; page 16 for a disclosure of oligonucleotide fragments and; page 18 for a definition of "complementary."

US Patent 5,445,934 is incorporated by reference into the specification as originally filed at page 60. Support for the above amendment to the specification is found in the incorporated US Patent 5,445,934 at columns 31 and 32.

The undersigned registered agent Linda T. Parker carried out a computer search of the nonredundant nucleotide database posted by the National Center for Biotechnology Information (NCBI)(ftp://ftp.ncbi.nlm.nih.gov/blast/db/ntz)) on November 3, 1999. The

computer search carried out was a BLASTN query using default parameters of SEQ ID NO: 5746 through SEQ ID NO: 8666.

A copy of the BLASTN output is on the enclosed CD-ROM. The BLASTN output can be read using a text editor such as "Multi-Edit" text editor available from American Cybernetics at http//www.amcyber.com or "Xemacs" text editor available from http://www.xemacs.org. The BLASTN output can be parsed using the Bio::Tools::Blast.pm module "_parse_stream" available from BioPerl at http://bioperl.org.

Based on analysis of the BLASTN output the original set of 2921 sequences was reduced by selecting only those sequences which were greater than 400 nucleotides and (a) had no matches to any public sequence in the queried database, or (b) matched for the top hit (best E value) http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/glossary2.html to a public sequence in the queried database in only a single high scoring segment pair http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/glossary2.html of less than 100 nucleotides where the match had an expectation (E value) greater than 1E-3. The original set of 2961 sequences was reduced to the subset of 497 sequences listed in the claims.

Applicants further submit that it should not be an undue burden on the Patent and Trademark Office to replicate such a BLASTN query. In particular applicants submit that such a relatively straightforward search of the 2921 sequences and the subsequent examination of claims 8-11 should not be a serious burden which would cause the PTO to seek to restrict limitations in applicants' claims to a small number of sequences. Any such sequence number restriction would be an undue hardship on applicants. Arrays of nucleic acid sequence are commonly employed where a single array on a solid support contains

thousands of separated nucleic acid sequence. To require an applicant to file hundreds of applications to cover a single product would serve only to effectively deprive applicant of patent rights on his invention.

Should the Examiner have any questions regarding this application, the Examiner is encouraged to contact Applicants' undersigned representative at (908) 684-8061.

Respectfully submitted,

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